



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 5, 2026 – 05:18 PM UTC

PDB ID : 6TYL / pdb_00006tyl
Title : Crystal structure of mammalian Ric-8A:Galpha(i):nanobody complex
Authors : Mou, T.C.; McClelland, L.; Yates-Hansen, C.; Sprang, S.R.
Deposited on : 2019-08-09
Resolution : 3.30 Å(reported)

This is a wwPDB X-ray Structure Validation Summary Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

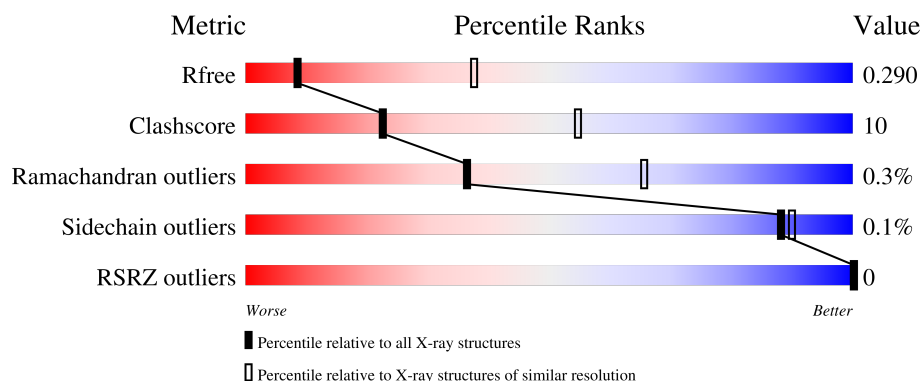
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.30 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



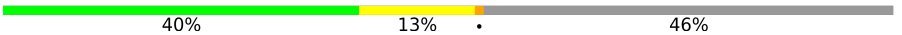
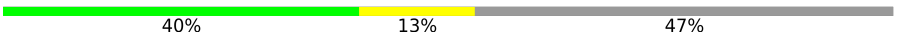
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	1169 (3.32-3.28)
Clashscore	190562	1209 (3.32-3.28)
Ramachandran outliers	187476	1188 (3.32-3.28)
Sidechain outliers	187428	1187 (3.32-3.28)
RSRZ outliers	180081	1169 (3.32-3.28)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	492	
1	F	492	
2	C	124	
2	H	124	
3	E	131	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
3	J	131	 68% 18% 14%
4	D	134	 75% 16% 10%
4	I	134	 77% 13% 10%
5	B	354	 40% 13% 46%
5	G	354	 40% 13% 47%

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 15938 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called Resistance to inhibitors of cholinesterase 8 homolog A (C. elegans).

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	484	Total	C	N	O	P	S	0	0	0
			3860	2424	684	728	2	22			
1	F	476	Total	C	N	O	P	S	0	0	0
			3793	2382	672	716	2	21			

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	0	GLY	-	expression tag	UNP B1H241
A	232	PHE	TYR	engineered mutation	UNP B1H241
F	0	GLY	-	expression tag	UNP B1H241
F	232	PHE	TYR	engineered mutation	UNP B1H241

- Molecule 2 is a protein called Nanobody A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	C	112	Total	C	N	O	S	0	0	0
			853	528	155	167	3			
2	H	111	Total	C	N	O	S	0	0	0
			847	525	154	165	3			

- Molecule 3 is a protein called Nanobody B.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	E	106	Total	C	N	O	S	0	0	0
			798	492	143	159	4			
3	J	113	Total	C	N	O	S	0	0	0
			850	523	155	168	4			

- Molecule 4 is a protein called Nanobody C.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	D	121	Total	C	N	O	S	0	0	0
			937	585	166	182	4			
4	I	121	Total	C	N	O	S	0	0	0
			937	585	166	182	4			

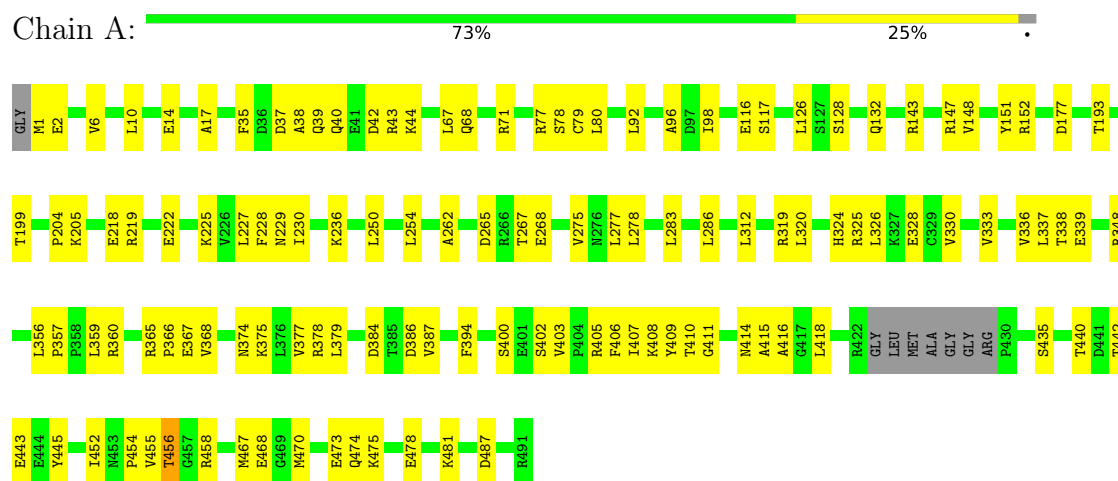
- Molecule 5 is a protein called Guanine nucleotide-binding protein G(i) subunit alpha-1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
5	B	190	Total	C	N	O	S	0	0	0
			1545	992	249	293	11			
5	G	187	Total	C	N	O	S	0	0	0
			1518	976	243	288	11			

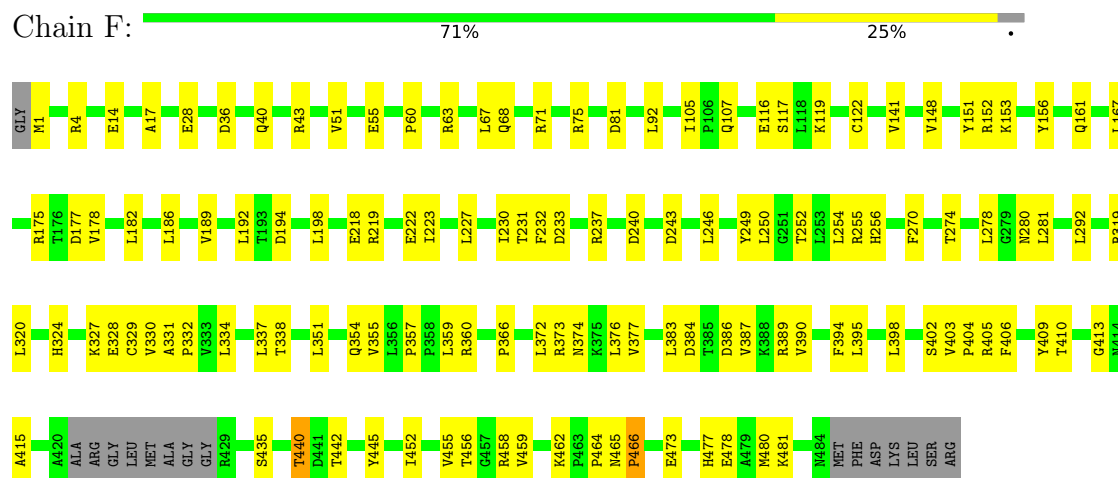
3 Residue-property plots

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

- Molecule 1: Resistance to inhibitors of cholinesterase 8 homolog A (*C. elegans*)



- Molecule 1: Resistance to inhibitors of cholinesterase 8 homolog A (*C. elegans*)



- Molecule 2: Nanobody A





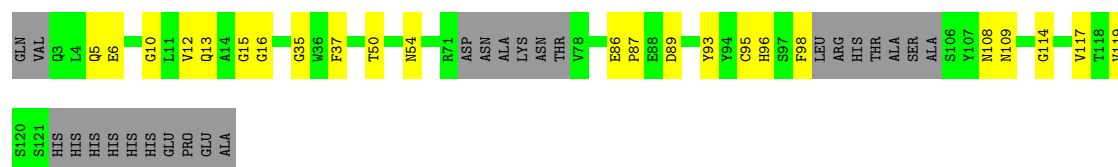
- Molecule 2: Nanobody A

Chain H: 65% 25% 10%



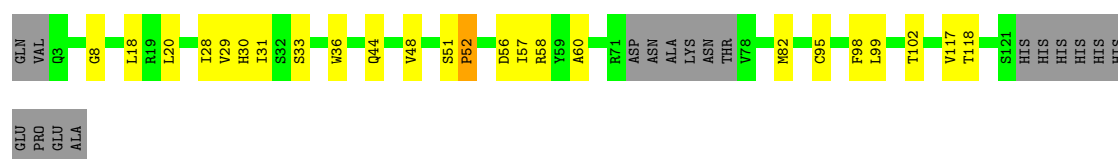
- Molecule 3: Nanobody B

Chain E: 63% 18% 19%



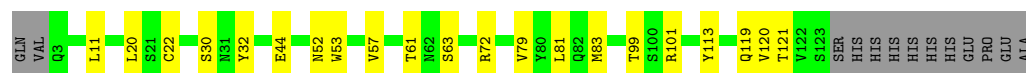
- Molecule 3: Nanobody B

Chain J: 68% 18% 14%



- Molecule 4: Nanobody C

Chain D: 75% 16% 10%

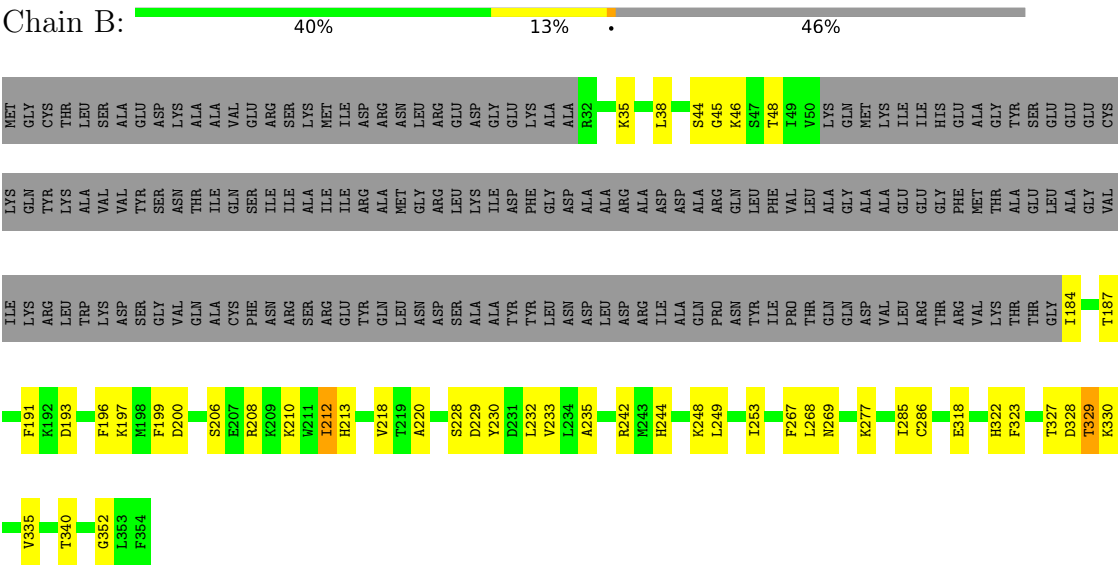


- Molecule 4: Nanobody C

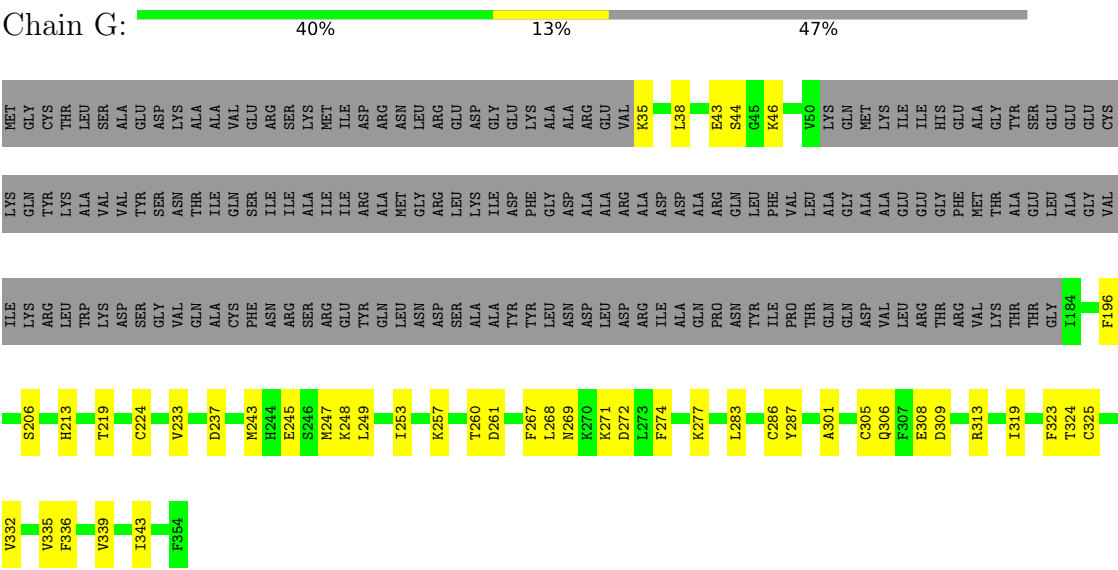
Chain I: 77% 13% 10%



- Molecule 5: Guanine nucleotide-binding protein G(i) subunit alpha-1



• Molecule 5: Guanine nucleotide-binding protein G(i) subunit alpha-1



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	93.05Å 144.73Å 114.42Å 90.00° 94.66° 90.00°	Depositor
Resolution (Å)	39.53 – 3.30 39.53 – 3.30	Depositor EDS
% Data completeness (in resolution range)	90.1 (39.53-3.30) 45.6 (39.53-3.30)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.46 (at 3.25Å)	Xtriage
Refinement program	PHENIX	Depositor
R, R_{free}	0.248 , 0.287 0.252 , 0.290	Depositor DCC
R_{free} test set	1975 reflections (4.19%)	wwPDB-VP
Wilson B-factor (Å ²)	91.9	Xtriage
Anisotropy	0.140	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 125.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.38$, $\langle L^2 \rangle = 0.21$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	15938	wwPDB-VP
Average B, all atoms (Å ²)	109.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.07% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: TPO, SEP

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	A	0.13	0/3901	0.35	0/5270
1	F	0.13	0/3833	0.32	0/5183
2	C	0.09	0/869	0.28	0/1178
2	H	0.11	0/863	0.33	0/1170
3	E	0.10	0/811	0.33	0/1092
3	J	0.11	0/865	0.34	0/1167
4	D	0.08	0/956	0.27	0/1295
4	I	0.08	0/956	0.26	0/1295
5	B	0.13	0/1575	0.32	0/2117
5	G	0.10	0/1548	0.29	0/2081
All	All	0.12	0/16177	0.32	0/21848

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	3860	0	3899	97	0
1	F	3793	0	3829	92	0
2	C	853	0	823	26	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	H	847	0	818	21	0
3	E	798	0	759	16	0
3	J	850	0	813	17	0
4	D	937	0	896	16	0
4	I	937	0	896	15	0
5	B	1545	0	1523	38	0
5	G	1518	0	1495	41	0
All	All	15938	0	15751	332	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 10.

The worst 5 of 332 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:B:212:ILE:HG22	5:B:213:HIS:H	1.24	1.02
1:A:357:PRO:HB2	4:D:53:TRP:HE1	1.45	0.81
1:A:262:ALA:H	1:A:267:THR:HG22	1.46	0.80
5:B:212:ILE:HG22	5:B:213:HIS:N	1.98	0.75
4:D:119:GLN:HG2	5:G:305:CYS:HB2	1.71	0.72

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	478/492 (97%)	432 (90%)	45 (9%)	1 (0%)	43	71
1	F	470/492 (96%)	421 (90%)	48 (10%)	1 (0%)	43	71
2	C	110/124 (89%)	96 (87%)	13 (12%)	1 (1%)	14	43
2	H	109/124 (88%)	99 (91%)	10 (9%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	E	100/131 (76%)	86 (86%)	14 (14%)	0	100	100
3	J	109/131 (83%)	96 (88%)	12 (11%)	1 (1%)	14	43
4	D	119/134 (89%)	110 (92%)	9 (8%)	0	100	100
4	I	119/134 (89%)	110 (92%)	9 (8%)	0	100	100
5	B	186/354 (52%)	158 (85%)	26 (14%)	2 (1%)	11	39
5	G	183/354 (52%)	160 (87%)	23 (13%)	0	100	100
All	All	1983/2470 (80%)	1768 (89%)	209 (10%)	6 (0%)	36	65

5 of 6 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	C	76	ASN
3	J	52	PRO
5	B	212	ILE
1	A	456	THR
1	F	466	PRO

5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	421/424 (99%)	421 (100%)	0	100	100
1	F	414/424 (98%)	414 (100%)	0	100	100
2	C	90/101 (89%)	90 (100%)	0	100	100
2	H	89/101 (88%)	89 (100%)	0	100	100
3	E	86/107 (80%)	86 (100%)	0	100	100
3	J	91/107 (85%)	91 (100%)	0	100	100
4	D	97/109 (89%)	97 (100%)	0	100	100
4	I	97/109 (89%)	97 (100%)	0	100	100
5	B	172/304 (57%)	171 (99%)	1 (1%)	78	81
5	G	169/304 (56%)	169 (100%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
All	All	1726/2090 (83%)	1725 (100%)	1 (0%)	88 90

All (1) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
5	B	329	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 17 such sidechains are listed below:

Mol	Chain	Res	Type
5	G	346	ASN
1	F	484	ASN
3	E	13	GLN
3	J	96	HIS
3	J	113	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

4 non-standard protein/DNA/RNA residues are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
1	SEP	F	435	1	8,9,10	1.61	1 (12%)	7,12,14	1.33	1 (14%)
1	TPO	F	440	1	8,10,11	1.11	0	10,14,16	2.24	1 (10%)
1	SEP	A	435	1	8,9,10	1.61	1 (12%)	7,12,14	1.35	1 (14%)
1	TPO	A	440	1	8,10,11	1.22	0	10,14,16	1.62	2 (20%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral

centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	SEP	F	435	1	-	3/6/8/10	-
1	TPO	F	440	1	-	0/9/11/13	-
1	SEP	A	435	1	-	4/6/8/10	-
1	TPO	A	440	1	-	5/9/11/13	-

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	F	435	SEP	P-O1P	3.52	1.61	1.50
1	A	435	SEP	P-O1P	3.51	1.61	1.50

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	F	440	TPO	P-OG1-CB	-6.49	105.68	123.33
1	A	440	TPO	CG2-CB-CA	-3.54	106.37	113.26
1	A	435	SEP	OG-CB-CA	2.94	111.01	108.14
1	F	435	SEP	OG-CB-CA	2.79	110.86	108.14
1	A	440	TPO	P-OG1-CB	-2.73	115.91	123.33

There are no chirality outliers.

5 of 12 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	A	435	SEP	N-CA-CB-OG
1	A	435	SEP	CB-OG-P-O1P
1	A	435	SEP	CB-OG-P-O2P
1	A	440	TPO	N-CA-CB-CG2
1	A	440	TPO	N-CA-CB-OG1

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	F	440	TPO	1	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data [i](#)

6.1 Protein, DNA and RNA chains [i](#)

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	482/492 (97%)	-1.78	0 100 100	42, 87, 154, 208	0
1	F	474/492 (96%)	-1.71	0 100 100	51, 105, 186, 222	0
2	C	112/124 (90%)	-1.72	0 100 100	55, 92, 145, 156	0
2	H	111/124 (89%)	-1.75	0 100 100	66, 94, 128, 155	0
3	E	106/131 (80%)	-1.62	0 100 100	84, 130, 166, 215	0
3	J	113/131 (86%)	-1.63	0 100 100	80, 118, 148, 169	0
4	D	121/134 (90%)	-1.75	0 100 100	64, 93, 122, 197	0
4	I	121/134 (90%)	-1.77	0 100 100	52, 94, 124, 161	0
5	B	190/354 (53%)	-1.75	0 100 100	45, 119, 178, 211	0
5	G	187/354 (52%)	-1.69	0 100 100	62, 151, 198, 245	0
All	All	2017/2470 (81%)	-1.73	0 100 100	42, 106, 175, 245	0

There are no RSRZ outliers to report.

6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled ‘Q< 0.9’ lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
1	SEP	F	435	10/11	0.99	0.02	135,140,148,149	0
1	TPO	F	440	11/12	0.99	0.03	168,170,175,177	0
1	SEP	A	435	10/11	1.00	0.01	109,126,155,158	0
1	TPO	A	440	11/12	1.00	0.02	86,117,141,148	0

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.